



# 9

## SEQUENCE LISTING

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TECH CENTER 1600/2900

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Shlomit, Edinger R.

<120> Novel GPCR-Like Proteins and Nucleic Acids Encoding  
Same

<130> 21402-224 AG

<140> 10/024444

<141> 2001-12-18

<150> 60/256635

<151> 2000-12-18

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 977

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Unknown

<400> 1

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atacatgttg gcactgacca gcaatggct gctgctccctg gccatcacca tagaagcccg 180  
gctccacatg cccatgttacc tcctgcttgg gcagctctct ctcatggacc tcctgttac 240  
atctgttgc actcccaagg ccttggcgga ctttctgcgc agagaaaaca ctatccctt 300  
tggaggctgt gcacttcaga tggccttgc actgacaatg gtagcgctg aggacctcct 360  
actggccttc atggcctatg acaggatgt ggcatttgt catcctctga aatacatgac 420  
cctcatgagc ccaagagtct gctggatcat ggtggccaca tcctggatcc tggcatccct 480  
gattgctata ggacatacca tgtacactat gcacccctt ttctgtgtgt cctggaaat 540  
caggcatctg ctctgtgaga tcccaccctt gctgaagttg gcctgtgctg atacccat 600  
gtatgagctt ataatacgt tgacagggtg gacttccctc ttgctccccca tttctgccc 660  
tgtggcctcc tacacactag tccttattcac tgtgcttctgt atgccatcaa atgagggggag 720  
gaagaaaagcc cttgtcacct gctcttccca cctgattgtg gtcggatgt tctatggagc 780  
tgccacatcc atgtatgtct tgcccaggcc cttccacagc cccaaacaag acaacatcat 840  
ctctgttttc tacacaatttgc tcactccagc cctgaatcca ctcatctaca gcctgaggaa 900  
taaggagggtc atgcgggcct tgaggagggt cctggaaaaa tacatactgc tggcacattc 960  
cacgctctag ggaagga 977

<210> 2  
<211> 316  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Unknown

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20 25 30  
  
Ile Leu Tyr Met Leu Ala Leu Thr Ser Asn Gly Leu Leu Leu Ala  
35 40 45  
  
Ile Thr Ile Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly  
50 55 60  
  
Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys  
65 70 75 80  
  
Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly  
85 90 95  
  
Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Ser Ala Glu Asp  
100 105 110  
  
Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
115 120 125  
  
Pro Leu Lys Tyr Met Thr Leu Met Ser Pro Arg Val Cys Trp Ile Met  
130 135 140  
  
Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ile Ala Ile Gly His Thr  
145 150 155 160  
  
Met Tyr Thr Met His Leu Pro Phe Cys Val Ser Trp Glu Ile Arg His  
165 170 175  
  
Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr  
180 185 190  
  
Ser Arg Tyr Glu Leu Ile Ile Tyr Val Thr Gly Val Thr Phe Leu Leu  
195 200 205  
  
Leu Pro Ile Ser Ala Ile Val Ala Ser Tyr Thr Leu Val Leu Phe Thr  
210 215 220  
  
Val Leu Arg Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr  
225 230 235 240  
  
Cys Ser Ser His Leu Ile Val Val Gly Met Phe Tyr Gly Ala Ala Thr

245

250

255

Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn  
260 265 270

Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu  
275 280 285

Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val  
290 295 300

Leu Gly Lys Tyr Ile Leu Leu Ala His Ser Thr Leu  
305 310 315

<210> 3

<211> 316

<212> PRT

<213> human

<400> 3

Met Glu Leu Trp Asn Phe Thr Leu Gly Ser Gly Phe Ile Leu Val Gly  
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Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Ile Thr  
20 25 30

Ile Leu Tyr Leu Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Ala  
35 40 45

Ile Thr Met Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly  
50 55 60

Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys  
65 70 75 80

Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly  
85 90 95

Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Gly Ala Glu Asp  
100 105 110

Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
115 120 125

Pro Leu Thr Tyr Met Thr Leu Met Ser Ser Arg Ala Cys Trp Leu Met  
130 135 140

Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Ile Tyr Thr  
145 150 155 160

Val Tyr Thr Met His Tyr Pro Phe Cys Arg Ala Gln Glu Ile Arg His  
165 170 175

Leu Leu Cys Glu Ile Pro His Leu Leu Lys Val Ala Cys Ala Asp Thr  
180 185 190

Ser Arg Tyr Glu Leu Met Val Tyr Val Met Gly Val Thr Phe Leu Ile  
 195 200 205  
 Pro Ser Leu Ala Ala Ile Leu Ala Ser Tyr Thr Gln Ile Leu Leu Thr  
 210 215 220  
 Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr  
 225 230 235 240  
 Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Ala Ala Thr  
 245 250 255  
 Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Thr Arg Gln Asp Asn  
 260 265 270  
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val  
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 Leu Gly Lys Tyr Met Leu Pro Ala His Ser Thr Leu  
 305 310 315

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 <212> PRT  
 <213> mouse

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 Ala Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Val  
 35 40 45  
 Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg  
 50 55 60  
 Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys  
 65 70 75 80  
 Ala Val Met Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Gly Gly  
 85 90 95  
 Cys Ala Leu Gln Met Ala Leu Ala Leu Met Leu Gly Ser Ala Glu Asp  
 100 105 110  
 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Asn Tyr Met Val Phe Met Ser Pro Thr Val Cys Trp Leu Ile  
 130 135 140

Val Ser Thr Ser Trp Ile Leu Ala Ser Leu Thr Ala Val Gly His Thr  
 145 150 155 160  
 Val Tyr Thr Met His Phe Pro Phe Cys Met Ser Gln Glu Ile Arg His  
 165 170 175  
 Leu Leu Cys Glu Ile Leu Pro Leu Leu Lys Leu Ser Cys Val Asp Thr  
 180 185 190  
 Ser Gln Tyr Glu Leu Met Val Tyr Val Thr Gly Val Thr Phe Leu Leu  
 195 200 205  
 Leu Pro Leu Ser Ala Ile Val Thr Ser Tyr Thr Leu Ile Leu Ser Thr  
 210 215 220  
 Val Leu His Met Pro Ser Asn Glu Gly Lys Lys Lys Ala Leu Val Thr  
 225 230 235 240  
 Cys Leu Ser His Leu Met Val Val Gly Met Phe Tyr Gly Ala Ala Thr  
 245 250 255  
 Phe Met Tyr Val Leu Pro Ser Ser Leu His Ser Ala Lys Gln Asp Asn  
 260 265 270  
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Leu Arg Arg Val  
 290 295 300  
 Leu Gly Arg Tyr Ile Leu Pro Ala His Leu Thr Leu  
 305 310 315  
  
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 <212> PRT  
 <213> mouse  
  
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 Met Glu Pro Trp Asn Ser Thr Leu Glu Ser Gly Phe Ile Leu Val Gly  
 1 5 10 15  
 Ile Leu Asp Gly Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Val Thr  
 20 25 30  
 Thr Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Val  
 35 40 45  
 Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg  
 50 55 60  
 Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Asn  
 65 70 75 80  
 Thr Val Val Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Glu Gly

85

90

95

Cys Ala Leu Gln Leu Phe Ser Ala Met Thr Leu Gly Gly Ala Glu Asp  
 100 105 110

Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125

Pro Leu Asn Tyr Met Ile Phe Met Ser Pro Lys Ala Cys Arg Leu Met  
 130 135 140

Val Ala Ile Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Gly His Thr  
 145 150 155 160

Val Tyr Thr Met His Phe Pro Phe Cys Met Ser Gln Glu Ile Arg His  
 165 170 175

Leu Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr  
 180 185 190

Ser Gln Tyr Glu Leu Met Val Tyr Val Thr Gly Val Ile Phe Leu Leu  
 195 200 205

Leu Pro Leu Ser Ala Ile Ile Thr Ser Tyr Ser Leu Ile Leu Phe Thr  
 210 215 220

Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr  
 225 230 235 240

Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Gly Ala Thr  
 245 250 255

Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn  
 260 265 270

Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu  
 275 280 285

Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Val Arg Arg Val  
 290 295 300

Leu Gly Arg His Ile Leu Pro Ala His Ala Thr Val  
 305 310 315

&lt;210&gt; 6

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; mouse

&lt;400&gt; 6

Met Glu Pro Trp Asn Ser Thr Leu Glu Ser Gly Phe Ile Leu Val Gly  
 1 5 10 15

Ile Leu Asp Gly Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Val Thr  
 20 25 30

Thr Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Leu Leu Val  
 35 40 45  
 Ile Thr Val Asp Ala Arg Leu His Val Pro Met Tyr Leu Leu Leu Arg  
 50 55 60  
 Gln Leu Ser Leu Ile Asp Leu Leu Phe Thr Ser Val Val Thr Pro Asn  
 65 70 75 80  
 Thr Val Val Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Glu Gly  
 85 90 95  
 Cys Ala Leu Gln Leu Phe Ser Ala Met Thr Leu Gly Gly Ala Glu Glu  
 100 105 110  
 Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
 115 120 125  
 Pro Leu Asn Tyr Met Ile Phe Met Ser Pro Lys Ala Cys Arg Leu Met  
 130 135 140  
 Val Ala Ile Ser Trp Ile Leu Ala Ser Leu Ser Ala Leu Gly His Thr  
 145 150 155 160  
 Val Tyr Thr Met His Phe Pro Phe Cys Met Ser Gln Glu Ile Arg His  
 165 170 175  
 Leu Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr  
 180 185 190  
 Ser Gln Tyr Glu Leu Met Val Tyr Val Thr Gly Val Ile Phe Leu Leu  
 195 200 205  
 Leu Pro Leu Ser Ala Ile Ile Thr Ser Tyr Ser Leu Ile Leu Phe Thr  
 210 215 220  
 Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr  
 225 230 235 240  
 Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Gly Ala Thr  
 245 250 255  
 Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn  
 260 265 270  
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu  
 275 280 285  
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Val Arg Arg Val  
 290 295 300  
 Leu Gly Arg His Ile Leu Pro Ala His Ala Thr Val  
 305 310 315

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<212> PRT  
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Ile Leu Asp Asp Ser Gly Ser Pro Glu Leu Leu Cys Ala Thr Phe Thr  
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Ala Leu Tyr Met Leu Ala Leu Ile Ser Asn Gly Leu Leu Ile Leu Val  
35 40 45  
  
Ile Thr Met Asp Ala Arg Leu His Val Pro Met Tyr Phe Leu Leu Gly  
50 55 60  
  
Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys  
65 70 75 80  
  
Ala Val Ile Asp Phe Leu Leu Arg Asp Asn Thr Ile Ser Phe Glu Gly  
85 90 95  
  
Cys Ser Leu Gln Met Phe Leu Ala Leu Thr Leu Gly Gly Ala Glu Asp  
100 105 110  
  
Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His  
115 120 125  
  
Pro Leu Asn Tyr Met Ile Phe Met Arg Pro Ser Ile Cys Trp Leu Met  
130 135 140  
  
Val Ala Thr Ser Trp Val Leu Ala Ser Leu Met Ala Leu Gly Tyr Thr  
145 150 155 160  
  
Thr Tyr Thr Met Gln Tyr Ser Tyr Cys Lys Ser Arg Lys Ile Arg His  
165 170 175  
  
Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr  
180 185 190  
  
Ser Lys Tyr Glu Leu Met Val Tyr Val Met Gly Val Thr Phe Leu Ile  
195 200 205  
  
Pro Pro Leu Ala Ala Ile Leu Ala Ser Tyr Ser Leu Ile Leu Phe Thr  
210 215 220  
  
Val Leu His Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr  
225 230 235 240  
  
Cys Ser Ser His Leu Thr Val Val Gly Met Phe Tyr Gly Ala Ala Thr  
245 250 255  
  
Phe Met Tyr Val Leu Pro Asn Ser Phe His Ser Pro Arg Gln Asp Asn  
260 265 270  
  
Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu  
275 280 285

Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Leu Ile Arg Val  
290 295 300

Leu Gly Arg Tyr Ile Val Pro Ala His Pro Thr Leu  
305 310 315

<210> 8  
<211> 17  
<212> PRT  
<213> Unknown Organism

<220>  
<223> Description of Unknown Organism: Protein motif

<220>  
<221> VARIANT  
<222> (1)  
<223> X1 wherein X aa is G, or S, or T, or A, or L, or  
I, or V, or M, or F, or Y, or W, or C

<220>  
<221> VARIANT  
<222> (2)  
<223> X2 wherein X aa is G, or S, or T, or A, or N, or  
C, or P, or D, or E

<220>  
<221> VARIANT  
<222> (3)  
<223> X3 wherein X aa is E, or D, or P, or K, or R, or H

<220>  
<221> VARIANT  
<222> (4)  
<223> X4 wherein X aa is any amino acid

<220>  
<221> VARIANT  
<222> (5)  
<223> X5 wherein X aa is any amino acid

<220>  
<221> VARIANT  
<222> (6)  
<223> X6 wherein X aa is L, or I, or V, or M, or N, or  
Q, or G, or A

<220>  
<221> VARIANT  
<222> (7)  
<223> X7 wherein X aa is any amino acid

<220>  
<221> VARIANT  
<222> (8)

<223> X8 wherein X is any amino acid

<220>

<221> VARIANT

<222> (9)

<223> X9 wherein X aa is L, or I, or V, or M, or F, or T

<220>

<221> VARIANT

<222> (10)

<223> X10 wherein Xaa is G, or S, or T, or A, or N, or C

<220>

<221> VARIANT

<222> (11)

<223> X11 wherein Xaa is L, or I, or V, or M, or F, or Y, or W, or S, or T, or A, or C

<220>

<221> VARIANT

<222> (12)

<223> X12 wherein X aa is D, or E, or N, or H

<220>

<221> VARIANT

<222> (14)

<223> X13 wherein X aa is F, or Y, or W, or C, or S, or H

<220>

<221> VARIANT

<222> (15)

<223> X14 wherein X aa is any amino acid

<220>

<221> VARIANT

<222> (16)

<223> X15 wherein X aa is any amino acid

<220>

<221> VARIANT

<222> (17)

<223> X16 wherein X aa is L, or I or V, or M

<400> 8  
Xaa Arg Xaa Xaa Xaa  
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Xaa

<210> 9  
<211> 254  
<212> PRT  
<213> Unknown Organism

<220>  
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 <222> (1)..(254)  
 <223> 7tm\_1,7 transmembrane receptor domain

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Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu  
 20 25 30

Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly  
 35 40 45

Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Val Gly Ala Leu Phe  
 50 55 60

Val Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile  
 65 70 75 80

Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg  
 85 90 95

Thr Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala  
 100 105 110

Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val  
 115 120 125

Glu Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser  
 130 135 140

Val Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Val Leu  
 145 150 155 160

Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu  
 165 170 175

Arg Lys Arg Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser  
 180 185 190

Glu Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Phe Val  
 195 200 205

Leu Cys Trp Leu Pro Tyr His Ile Val Leu Leu Asp Ser Leu Cys  
 210 215 220

Leu Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu  
 225 230 235 240

Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr  
 245 250

<210> 10  
 <211> 22

<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: PCR Primer

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tgccacatTC atgtatgtct tg

22

<210> 11  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

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cacagccccca aacaagacaa catcat

26

<210> 12  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

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ggctggagtG acaattgtgt ag

22